

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 09/841,963 A

CRF Processing Date: 2/21/2002
 Edited by: [Signature]
 Verified by: [Signature] (STIC staff)

ENTERED

TECH CENTER 1600/2900

FEB 5 2002

RECEIVED

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number input by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☒ Corrected an obvious error in the response, specifically: 21507 response
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95



1600

RAW SEQUENCE LISTING

DATE: 02/21/2002

PATENT APPLICATION: US/09/841,963A

TIME: 22:29:38

Input Set : N:\Cr3\02132002\I841963A.raw

Output Set: N:\CRF3\02212002\I841963A.raw

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1 <110> APPLICANT: Watson, Dennis K.
2   Papas, Takis S. (Deceased)
3   Papas, Tula C. (Legal Representative)
4 <120> TITLE OF INVENTION: Methods and compositions for the diagnosis and
5   treatment of cancer
6   based on transcription factor ETS2
7 <130> FILE REFERENCE: 10545-015-999
C--> 8 <140> CURRENT APPLICATION NUMBER: US/09/841,963A
9 <141> CURRENT FILING DATE: 2001-04-25
10 <150> PRIOR APPLICATION NUMBER: PCT/US99/27805
11 <151> PRIOR FILING DATE: 1999-11-23
12 <150> PRIOR APPLICATION NUMBER: 60/109,850
13 <151> PRIOR FILING DATE: 1998-11-25
14 <160> NUMBER OF SEQ ID NOS: 6
15 <170> SOFTWARE: PatentIn version 3.0
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 1894
19 <212> TYPE: DNA
20 <213> ORGANISM: Homo sapiens
21 <220> FEATURE:
22 <221> NAME/KEY: CDS
23 <222> LOCATION: (416)..(1423)
24 <400> SEQUENCE: 1
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27   ccagcaggca gccctgggct gggggtaggg gactccctac aggcacgcag cctgagaccc      180
28   gccaccagcc accccttgag ggtggccagg cccccagtgg ccaacctgag tgctgcctct      240
29   gccaccagcc ctgctggccc ctggttcgcg tggccccca gatgcctggc tgagacacgc      300
30   cagtggcctc agctgccac acctcttccc ggccctgga gttggcactg cagcagacag      360
31   ctccctgggc accaggcagc taacagacac agccgccagc ccaaacagca gcggc atg      418
32                                     Met
33                                     1
34   ggc agc gcc agc ccg ggt ctg agc agc gta tcc ccc agc cac ctc ctg      466
35   Gly Ser Ala Ser Pro Gly Leu Ser Ser Val Ser Pro Ser His Leu Leu
36                                     5          10          15
37   ctg ccc ccc gac acg gtg tgc cgg aca ggc ttg gag aag gcg gca gcg      514
38   Leu Pro Pro Asp Thr Val Ser Arg Thr Gly Leu Glu Lys Ala Ala Ala
39                                     20          25          30
40   ggg gca gtg ggt ctc gag aga cgg gac tgg agt ccc agt cca ccc gcc      562
41   Gly Ala Val Gly Leu Glu Arg Arg Asp Trp Ser Pro Ser Pro Pro Ala
42                                     35          40          45
43   acg ccc gag cag ggc ctg tcc gcc ttc gac ctc tcc tac ttt gac atg      610
44   Thr Pro Glu Gln Gly Leu Ser Ala Phe Asp Leu Ser Tyr Phe Asp Met

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45	50	55	60	65	
46	ctg tac cct gag gac agc agc tgg gca gcc aag gcc cct ggg gcc agc	658			
47	Leu Tyr Pro Glu Asp Ser Ser Trp Ala Ala Lys Ala Pro Gly Ala Ser				
48	70	75	80		
49	agt cgg gag gag cca cct gac cag cct gag cag tgc ccg gtc att gac	706			
50	Ser Arg Glu Glu Pro Pro Asp Gln Pro Glu Gln Cys Pro Val Ile Asp				
51	85	90	95		
52	agc caa gcc cca gcg ggc acc ctg gac ttg gtg ccc ggc ggg ctg acc	754			
53	Ser Gln Ala Pro Ala Gly Thr Leu Asp Leu Val Pro Gly Gly Leu Thr				
54	100	105	110		
55	ttg gag gag cac tcg ctg gag cag gtg cag tcc atg gtg gtg ggc gaa	802			
56	Leu Glu Glu His Ser Leu Glu Gln Val Gln Ser Met Val Val Gly Glu				
57	115	120	125		
58	gtg ctc aag gac atc gag acg gcc tgc aag ctg ctc aac atc acc gca	850			
59	Val Leu Lys Asp Ile Glu Thr Ala Cys Lys Leu Leu Asn Ile Thr Ala				
60	130	135	140	145	
61	gat ccc atg gac tgg agc ccc agc aat gtg cag aag tgg ctc ctg tgg	898			
62	Asp Pro Met Asp Trp Ser Pro Ser Asn Val Gln Lys Trp Leu Leu Trp				
63	150	155	160		
64	aca gag cac caa tac cgg ctg ccc ccc atg ggc aag gcc ttc cag gag	946			
65	Thr Glu His Gln Tyr Arg Leu Pro Pro Met Gly Lys Ala Phe Gln Glu				
66	165	170	175		
67	ctg gcg ggc aag gag ctg tgc gcc atg tcg gag gag cag ttc cgc cag	994			
68	Leu Ala Gly Lys Glu Leu Cys Ala Met Ser Glu Glu Gln Phe Arg Gln				
69	180	185	190		
70	cgc tcg ccc ctg ggt ggg gat gtg ctg cac gcc cac ctg gac atc tgg	1042			
71	Arg Ser Pro Leu Gly Gly Asp Val Leu His Ala His Leu Asp Ile Trp				
72	195	200	205		
73	aag tca gcg gcc tgg atg aaa gag cgg act tca cct ggg gcg att cac	1090			
74	Lys Ser Ala Ala Trp Met Lys Glu Arg Thr Ser Pro Gly Ala Ile His				
75	210	215	220	225	
76	tac tgt gcc tcg acc agt gag gag agc tgg acc gac agc gag gtg gac	1138			
77	Tyr Cys Ala Ser Thr Ser Glu Glu Ser Trp Thr Asp Ser Glu Val Asp				
78	230	235	240		
79	tca tca tgc tcc ggg cag ccc atc cac ctg tgg cag ttc ctc aag gag	1186			
80	Ser Ser Cys Ser Gly Gln Pro Ile His Leu Trp Gln Phe Leu Lys Glu				
81	245	250	255		
82	ttg cta ctc aag ccc cac agc tat ggc cgc ttc att agg tgg ctc aac	1234			
83	Leu Leu Leu Lys Pro His Ser Tyr Gly Arg Phe Ile Arg Trp Leu Asn				
84	260	265	270		
85	aag gag aag ggc atc ttc aaa att gag gac tca gcc cag gtg gcc cgg	1282			
86	Lys Glu Lys Gly Ile Phe Lys Ile Glu Asp Ser Ala Gln Val Ala Arg				
87	275	280	285		
88	ctg tgg ggc atc cgc aag aac cgt ccc gcc atg aac tgc gac aag ctg	1330			
89	Leu Trp Gly Ile Arg Lys Asn Arg Pro Ala Met Asn Cys Asp Lys Leu				
90	290	295	300	305	
91	agc cgc tcc atc cgc cag tct tac aag aag ggc atc atc cgg aag cca	1378			
92	Ser Arg Ser Ile Arg Gln Ser Tyr Lys Lys Gly Ile Ile Arg Lys Pro				
93	310	315	320		

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Input Set : N:\Crif3\02132002\I841963A.raw

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94      gac atc tcc cag cgc ctg gtc tac cag ttc gtg cac ccc atc tga      1423
95      Asp Ile Ser Gln Arg Leu Val Tyr Gln Phe Val His Pro Ile
96              325                      330                      335
97      gtgcctggcc cagggcctga aaccgcctc caggggcctc tctcctgcct gccctgcctc      1483
98      agccaggccc tgagatgggg gaaaacgggc agtgtgctct gctgctctga ccttcagag      1543
99      cccaaggcca gggaggggca accaactgcc ccagggggat atgggtcctc tggggccttc      1603
100     gggaccatgg ggcaggggtg ctctcctcctc agggccagct gctcccctgg aggacagagg      1663
101     gagacagggc tgcctcccaa cacctgcctc tgacccacagc atttcagag cagagcctac      1723
102     agaagggcag tgactcgaca aaggccacag gcagtccagg cctctctctg ctccatcccc      1783
103     ctgcctccca ttctgcacca cacctggcat ggtgcaggga gacatctgca cccctcagtt      1843
104     gggcagccag gagtgcctcc gggaatggat aataaagata ctagagaact g      1894
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107 <211> LENGTH: 335
108 <212> TYPE: PRT
109 <213> ORGANISM: Homo sapiens
110 <400> SEQUENCE: 2
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112     1              5              10              15
113     Leu Leu Pro Pro Asp Thr Val Ser Arg Thr Gly Leu Glu Lys Ala Ala
114             20              25              30
115     Ala Gly Ala Val Gly Leu Glu Arg Arg Asp Trp Ser Pro Ser Pro Pro
116             35              40              45
117     Ala Thr Pro Glu Gln Gly Leu Ser Ala Phe Asp Leu Ser Tyr Phe Asp
118             50              55              60
119     Met Leu Tyr Pro Glu Asp Ser Ser Trp Ala Ala Lys Ala Pro Gly Ala
120             65              70              75              80
121     Ser Ser Arg Glu Glu Pro Pro Asp Gln Pro Glu Gln Cys Pro Val Ile
122             85              90              95
123     Asp Ser Gln Ala Pro Ala Gly Thr Leu Asp Leu Val Pro Gly Gly Leu
124             100             105             110
125     Thr Leu Glu Glu His Ser Leu Glu Gln Val Gln Ser Met Val Val Gly
126             115             120             125
127     Glu Val Leu Lys Asp Ile Glu Thr Ala Cys Lys Leu Leu Asn Ile Thr
128             130             135             140
129     Ala Asp Pro Met Asp Trp Ser Pro Ser Asn Val Gln Lys Trp Leu Leu
130             145             150             155             160
131     Trp Thr Glu His Gln Tyr Arg Leu Pro Pro Met Gly Lys Ala Phe Gln
132             165             170             175
133     Glu Leu Ala Gly Lys Glu Leu Cys Ala Met Ser Glu Glu Gln Phe Arg
134             180             185             190
135     Gln Arg Ser Pro Leu Gly Gly Asp Val Leu His Ala His Leu Asp Ile
136             195             200             205
137     Trp Lys Ser Ala Ala Trp Met Lys Glu Arg Thr Ser Pro Gly Ala Ile
138             210             215             220
139     His Tyr Cys Ala Ser Thr Ser Glu Glu Ser Trp Thr Asp Ser Glu Val
140             225             230             235             240
141     Asp Ser Ser Cys Ser Gly Gln Pro Ile His Leu Trp Gln Phe Leu Lys
142             245             250             255
143     Glu Leu Leu Leu Lys Pro His Ser Tyr Gly Arg Phe Ile Arg Trp Leu

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144          260          265          270
145      Asn Lys Glu Lys Gly Ile Phe Lys Ile Glu Asp Ser Ala Gln Val Ala
146          275          280          285
147      Arg Leu Trp Gly Ile Arg Lys Asn Arg Pro Ala Met Asn Cys Asp Lys
148          290          295          300
149      Leu Ser Arg Ser Ile Arg Gln Ser Tyr Lys Lys Gly Ile Ile Arg Lys
150          305          310          315          320
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152          325          330          335
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155 <211> LENGTH: 1704
156 <212> TYPE: DNA
157 <213> ORGANISM: Mus sp.
158 <220> FEATURE:
159 <221> NAME/KEY: CDS
160 <222> LOCATION: (362)..(1336)
161 <400> SEQUENCE: 3
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164      tagacctgca ggcctgaggc ctcagactca cactcaaggg gcaagaggcc ctggtggccc      180
165      acctaaagac cacctctgtc ccagccctg ctgccccact gatgtctgac tgagaccag      240
166      cagtgaacct gagctgcctg cccactgcct cctcctggtc cctgagggtg gctctgccga      300
167      ggaaggacga ctcttctgaa gcaggcggct aacggaagca gcccgaagcc tccaccgcag      360
168      c atg ggc agt gcc agc cca ggc ctg agc aac gtg tcc ccc ggt tgc ctg      409
169      Met Gly Ser Ala Ser Pro Gly Leu Ser Asn Val Ser Pro Gly Cys Leu
170      1          5          10          15
171      cta ctg ttc cca gat gtg gca cca cga aca ggg acg gag aag gca gca      457
172      Leu Leu Phe Pro Asp Val Ala Pro Arg Thr Gly Thr Glu Lys Ala Ala
173          20          25          30
174      tca gga gca atg ggc cct gag aag cag gaa tgg agt cct agt cca ccc      505
175      Ser Gly Ala Met Gly Pro Glu Lys Gln Glu Trp Ser Pro Ser Pro Pro
176          35          40          45
177      gcc acc cct gag cag ggc ctg tct gct ttc tac ctc tct tac ttt aac      553
178      Ala Thr Pro Glu Gln Gly Leu Ser Ala Phe Tyr Leu Ser Tyr Phe Asn
179          50          55          60
180      atg tat ccc gac gat agc agc tgg gtc gcc aaa gtc ccc gag gcc cgt      601
181      Met Tyr Pro Asp Asp Ser Ser Trp Val Ala Lys Val Pro Glu Ala Arg
182          65          70          75          80
183      gcc ggg gag gac cac ccg gag gag ccc gag cag tgt ccc gtc att gac      649
184      Ala Gly Glu Asp His Pro Glu Glu Pro Glu Gln Cys Pro Val Ile Asp
185          85          90          95
186      agc cag gcc tct ggg agc acg ttg gat gag cac tcg cta gag cag gtg      697
187      Ser Gln Ala Ser Gly Ser Thr Leu Asp Glu His Ser Leu Glu Gln Val
188          100          105          110
189      caa tcg atg gtt gtg ggc gag gtc ctg aaa gat att gag acg gcc tgc      745
190      Gln Ser Met Val Val Gly Glu Val Leu Lys Asp Ile Glu Thr Ala Cys
191          115          120          125
192      aag ctt gtg aac atc aca gca gac cct ggg gac tgg agc cct ggt aac      793
193      Lys Leu Val Asn Ile Thr Ala Asp Pro Gly Asp Trp Ser Pro Gly Asn

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Input Set : N:\Crif3\02132002\I841963A.raw

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194          130          135          140
195      gtg cag aag tgg ctt tta tgg aca gaa cac cag tac cgg ctg cct cca      841
196      Val Gln Lys Trp Leu Leu Trp Thr Glu His Gln Tyr Arg Leu Pro Pro
197          145          150          155          160
198      gca ggc aag gcc ttc cag gag ctg ggc ggt aag gag ctg tgc gcc atg      889
199      Ala Gly Lys Ala Phe Gln Glu Leu Gly Gly Lys Glu Leu Cys Ala Met
200          165          170          175
201      tcc gag gaa cag ttc cgt cag cgt gca ccc ttg ggt ggg gat gta ctg      937
202      Ser Glu Glu Gln Phe Arg Gln Arg Ala Pro Leu Gly Gly Asp Val Leu
203          180          185          190
204      cat gcc cac ctg gac atc tgg aag tca gcg gcc tgg atg aag gag agg      985
205      His Ala His Leu Asp Ile Trp Lys Ser Ala Ala Trp Met Lys Glu Arg
206          195          200          205
207      acc tcg cct ggg acc ctt cac tac tgc gcc tcc acc agc gag gac ggc      1033
208      Thr Ser Pro Gly Thr Leu His Tyr Cys Ala Ser Thr Ser Glu Asp Gly
209          210          215          220
210      tgg acg gat ggt gag gtg gac tcg tcg tgc tcc ggg cag ccc att cac      1081
211      Trp Thr Asp Gly Glu Val Asp Ser Ser Cys Ser Gly Gln Pro Ile His
212          225          230          235          240
213      ctg tgg cag ttc ctg aaa gaa ctg ctg ctc aag ccc cac agc tat ggc      1129
214      Leu Trp Gln Phe Leu Lys Glu Leu Leu Lys Pro His Ser Tyr Gly
215          245          250          255
216      cgc ttc atc cgg tgg ggt gtg cgc aag aac cgg cca gcc atg aac tat      1177
217      Arg Phe Ile Arg Trp Gly Val Arg Lys Asn Arg Pro Ala Met Asn Tyr
218          260          265          270
219      gat aaa cta aga agc tcc atc cgc tgg ctc aac aag gag aaa ggc atc      1225
220      Asp Lys Leu Arg Ser Ser Ile Arg Trp Leu Asn Lys Glu Lys Gly Ile
221          275          280          285
222      ttc aaa att gag gac tca gca cag gtg gcc cga ctc cag tat tac aag      1273
223      Phe Lys Ile Glu Asp Ser Ala Gln Val Ala Arg Leu Gln Tyr Tyr Lys
224          290          295          300
225      aag ggc atg att cgt aaa ccc gcc atc tct cag cgc ctt gtc tac caa      1321
226      Lys Gly Met Ile Arg Lys Pro Ala Ile Ser Gln Arg Leu Val Tyr Gln
227          305          310          315          320
228      ttt gtg cat cca gtc tgagagccac agagaccaga ggcctacaac ctgccccagg      1376
229      Phe Val His Pro Val
230          325
231      cagccactct ctggttggcc tggctctctc tgetcactct gaattcaggg gctgctggta      1436
232      tcccagaacc caaggtccca gatagacagc cactgatcta cccatacaca tgagctctct      1496
233      gggtcataca caggccccag gaagatcgag ggagctagtt cagcacacag ggactggacc      1556
234      aagtcagctc accggacagt gatgtcactg gtctctgctc ctgccacaat cctgtaccat      1616
235      atctggcatg gtgctaagag atgtctgtac cctgcgttgg gaagccaggg gtgccctggg      1676
236      gatggataat aaagacgtaa gataactg      1704
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239 <211> LENGTH: 325
240 <212> TYPE: PRT
241 <213> ORGANISM: Mus sp.
242 <400> SEQUENCE: 4
243      Met Gly Ser Ala Ser Pro Gly Leu Ser Asn Val Ser Pro Gly Cys Leu

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VERIFICATION SUMMARY

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Input Set : N:\Crf3\02132002\I841963A.raw

Output Set: N:\CRF3\02212002\I841963A.raw

L:8 M:270 C: Current Application Number differs, Wrong Format